FIG.1

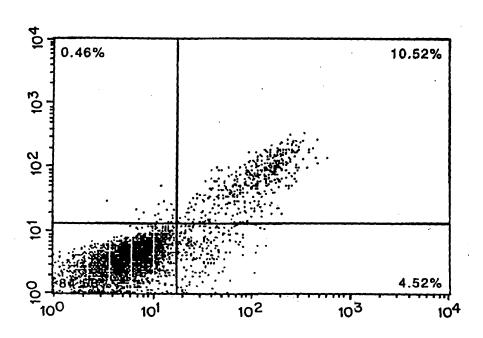


FIG. 2

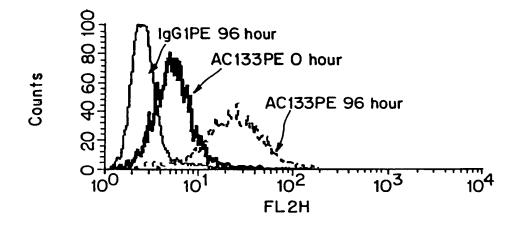


FIG. 3

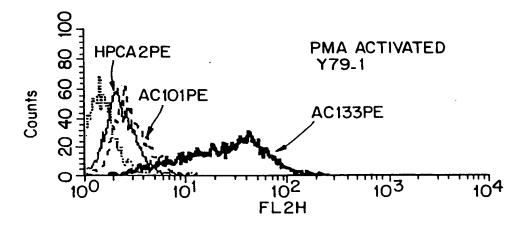


FIG.4A

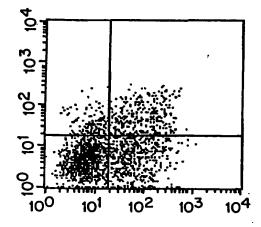
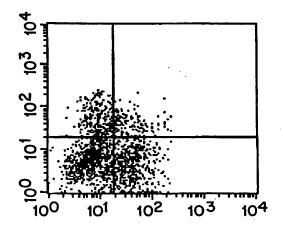
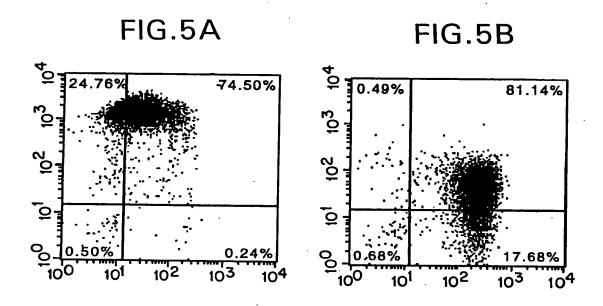


FIG.4B





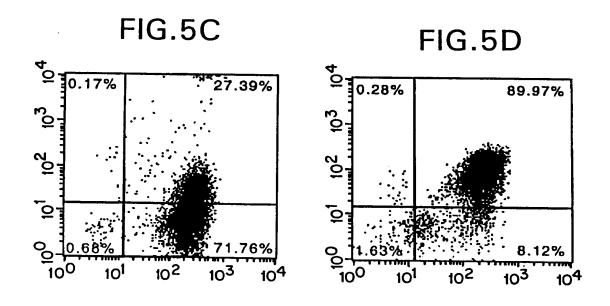


FIG.6

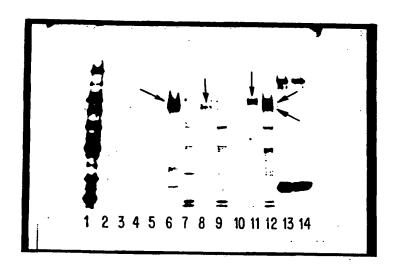


FIG. 7A

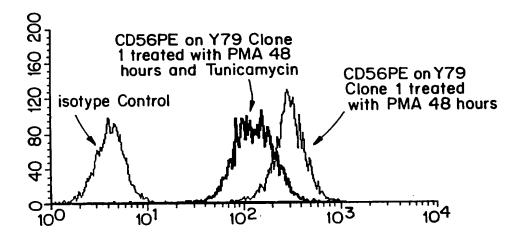


FIG. 7B

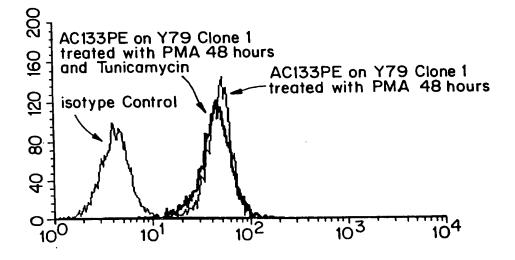


FIG.8

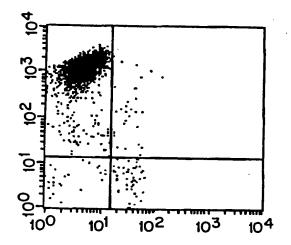


FIG.9A

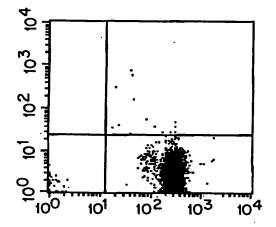


FIG.9B

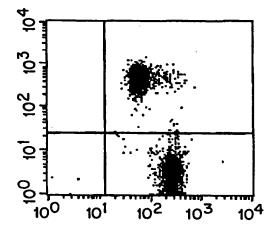
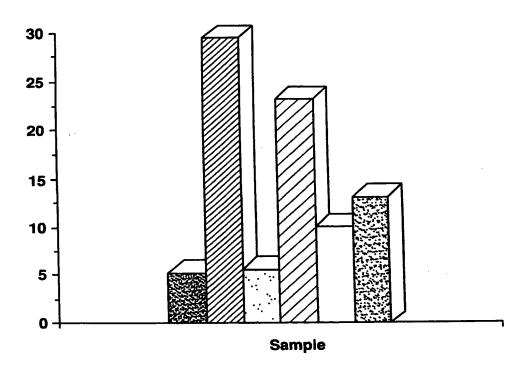
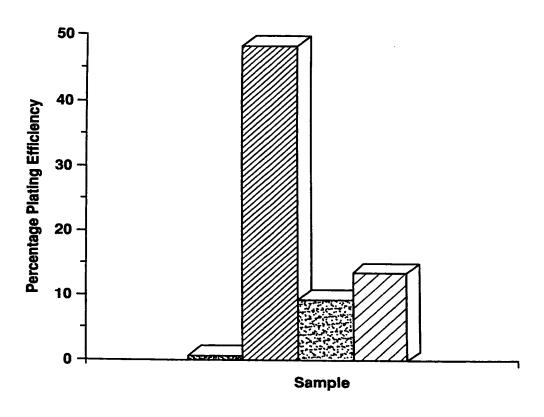


FIG.10



- **図 LP Control/CFU-GM**
- ☑ LP Control/BFU-E
- C4-AC101/CFU-GM
- C4-AC101/BFU-E
- C4-AC133/CFU-GM
- C4-AC133/BFU-E

FIG.11



- AC101/CFU-GM
- AC101/BFU-E
- AC133/CFU-GM
- AC133/BFU-E

CCA	AGTT	CTA	CCTC	ATGT	TT G	GAGG	ATCT	r GC	ragc	Me			_		GGC Gly	55
												TCA Ser				103
			Thr									GAA Glu 35				151
												CCC Pro				199
												CAG Gln				247
												GCA Ala				295
												GGT Gly				343
												CTG Leu 115				391
												TGT Cys				439
												CAG Gln				487
Glγ	Pro	Phe	Leu	Arg 155	Lys	Cys	Phe	Ala	11e 160	Ser	Leu	TTG Leu	Val	11e	Cys	535
Ile	Ile	Ile	Ser 170	Ile	Gly	Ile	Phe	Tyr 175	Gly	Phe	Val	GCA Ala	Asn 180	His	Gln	583
												GAT Asp 195	Ser			631
Lys	Asp 200	Leu	Arg	Thr	Leu	Leu 205	Asn	Glu	Thr	Pro	Glu 210	Gln	Ile	Lys		679
ATA Ile 215	TTG Leu	GCC Ala	CAG Gln	TAC Tyr	AAC Asn 220	ACT	ACC	AAG Lys	GAC Asp	AAG Lys 225	Ala	TTC Phe	ACA Thr	GAT Asp	CTG Leu 230	727

						Ile		GAC Asp			775
								ATG Met			823
								AGC Ser 275			871
								CTG Leu			919
								TGC Cys			967
								CTA Leu			1015
								GAT Asp			1063
	_							GGC Gly 355			1111
		_						GTA Val	_	_	1159
								AAT Asn			1207
								CAG Gln			1255
								TAC Tyr			1303
								TGG Trp 435			1351
	Ile							Phe		CTG Leu	1399
							His			ACC Thr 470	1447

ACC	CGA Arg	GGC	TGT Cys	GTC Val 475	Ser	AAC Asn	ACC Thr	GGA Gly	GGC Gly 480	GTC Val	TTC Phe	CTC Leu	ATG Met	GTT Val 485	GGA Gly	1495
GT1 Val	GGA Gly	Leu	AGT Ser 490	Phe	CTC Leu	TTT	TGC Cys	TGG Trp 495	ATA Ile	TTG Leu	ATG Met	ATC Ile	ATT Ile 500	GTG Val	GTT Val	1543
CTI	ACC Thr	Phe 505	GTC Val	TTT Phe	GGT Gly	GCA Ala	AAT Asn 510	GTG Val	GAA Glu	AAA Lys	CTG Leu	ATC Ile 515	TGT Cys	GAA Glu	CCT Pro	1591
TAC	ACG Thr 520	Ser	AAG Lys	GAA Glu	TTA Leu	TTC Phe 525	CGG Arg	GTT Val	TTG Leu	GAT Asp	ACA Thr 530	CCC Pro	TAC Tyr	TTA Leu	CTA Leu	1639
AAT Asn 535	GAA Glu	GAC Asp	TGG Trp	GAA Glu	TAC Tyr 540	TAT Tyr	CTC Leu	TCT Ser	GGG Gly	AAG Lys 545	CTA Leu	TTT Phe	AAT Asn	AAA Lys	TCA Ser 550	1687
AAA Lys	ATG Met	AAG Lys	CTC Leu	ACT Thr 555	TTT Phe	GAA Glu	CAA Gln	GTT Val	TAC Tyr 560	AGT Ser	GAC Asp	TGC Cys	AAA Lys	AAA Lys 565	AAT Asn	1735
AGA Arg	GGC	ACT Thr	TAC Tyr 570	GGC Gly	ACT Thr	CTT Leu	CAC His	CTG Leu 575	CAG Gln	AAC Asn	AGC Ser	TTC Phe	AAT Asn 580	ATC Ile	Ser	1783
GAA Glu	CAT His	CTC Leu 585	AAC Asn	ATT Ile	AAT Asn	GAG Glu	CAT His 590	ACT Thr	GGA Gly	AGC Ser	ATA Ile	AGC Ser 595	AGT Ser	GAA Glu	TTG Leu	1831
GAA Glu	AGT Ser 600	CTG Leu	AAG Lys	GTA Val	TAA naA	CTT Leu 605	TAA neA	ATC Ile	TTT Phe	CTG Leu	TTG Leu 610	GGT	GCA Ala	GCA Ala	GGA Gly	1879
AGA Arg 615	AAA Lys	AAC Asn	CTT Leu	CAG Gln	GAT Asp 620	TTT Phe	GCT Ala	GCT Ala	TGT Cys	GGA Gly 625	ATA Ile	GAC Asp	AGA Arg	ATG Met	AAT Asn 630	1927
TAT Tyr	GAC Asp	AGC Ser	TAC Tyr	TTG Leu 635	GCT Ala	CAG Gln	ACT Thr	GGT Gly	AAA Lys 640	TCC Ser	CCC Pro	GCA Ala	GGA Gly	GTG Val 645	AAT Asn	1975
			TTT Phe 650													2023
			TTG Leu													2071
			CAG Gln													2119
			AGC Ser													2167
			ACT Thr													2215

ATC ACA AAC AAT ACT TCC TCT GTT ATT ATT GAG GAA ACT AAG AAG TAT Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr 730 735 740	2263
GGG AGA ACA ATA ATA GGA TAT TTT GAA CAT TAT CTG CAG TGG ATC GAG Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu 745 750 755	2311
TTC TCT ATC AGT GAG AAA GTG GCA TCG TGC AAA CCT GTG GCC ACC GCT Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala 760 765 770	2359
CTA GAT ACT GCT GTT GAT GTC TTT CTG TGT AGC TAC ATT ATC GAC CCC Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro 785 780 785	2407
TTG AAT TTG TTT TGG TTT GGC ATA GGA AAA GCT ACT GTA TTT TTA CTT Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu 795 800 805	2455
CCG GCT CTA ATT TTT GCG GTA AAA CTG GCT AAG TAC TAT CGT CGA ATG Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met 810 820	2503
GAT TCG GAG GAC GTG TAC GAT GAT GTT GAA ACT ATA CCC ATG AAA AAT Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn 825 830 835	2551
ATG GAA AAT GGT AAT AAT GGT TAT CAT AAA GAT CAT GTA TAT GGT ATT Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile 840 845	2599
CAC AAT CCT GTT ATG ACA AGC CCA TCA CAA CAT T GATAGCTGAT His Asn Pro Val Met Thr Ser Pro Ser Gln His 855 860 865	2643
STTGAAACTG CTTGAGCATC AGGATACTCA AAGTGGAAAG GATCACAGAT TTTTGGTAGT	2703
TTCTGGGTCT ACAAGGACTT TCCAAATCCA GGAGCAACGC CAGTGGCAAC GTAGTGACTC	2763
AGGCGGGCAC CAAGGCAACG GCACCATTGG TCTCTGGGTA GTGCTTTAAG AATGAACACA	2823
ATCACGTTAT AGTCCATGGT CCATCACTAT TCAAGGATGA CTCCCTCCCT TCCTGTCTAT	2883
TTTTGTTTTT TACTTTTTTA CACTGAGTTT CTATTTAGAC ACTACAACAT ATGGGGTGTT	2943
GTTCCCATT GGATGCATTT CTATCAAAAC TCTATCAAAT GTGATGGCTA GATTCTAACA	3003
PATTGCCATG TGTGGAGTGT GCTGAACACA CACCAGTTTA CAGGAAAGAT GCATTTTGTG	3063
PACAGTAAAC GGTGTATATA CCTTTTGTTA CCACAGAGTT TTTTAAACAA ATGAGTATTA	3123
AGGACTITC TICTAAATGA GCTAAATAAG TCACCATTGA CTICTTGGTG CTGTTGAAAA	3183
AATCCATTT TCACTAAAAG TGTGTGAAAC CTACAGCATA TTCTTCACGC AGAGATTTTC	3243
TCTATTATA CTTTATCAAA GATTGGCCAT GTTCCACTTG GAAATGGCAT GCAAAAGCCA	3303
CATAGAGAA ACCTGCGTAA CTCCATCTGA CAAATTCAAA AGAGAGAGAG AGATCTTGAG	3363
GAGAAATGC TGTTCGTTCA AAAGTGGAGT TGTTTTAACA GATGCCAATT ACGGTGTACA	3423

GTTTAAC	AGA	GTTTTCTGTT	GCATTAGGAT	AAACATTAAT	TGGAGTGCAG	CTAACATGAG	3483
TATCATC	AGA	CTAGTATCAA	GTGTTCTAAA	ATGAAATATG	AGAAGATCCT	GTCACAATTC	3543
TTAGATC	TGG	TGTCCAGCAT	GGATGAAACC	TTTGAGTTTG	GTCCCTAAAT	TTGCATGAAA	3603
GCACAAGG	GTA	AATATTCATT	TGCTTCAGGA	GTTTCATGTT	GGATCTGTCA	TTATCAAAAG	3663
TGATCAG	CAA	TGAAGAACTG	GTCGGACAAA	ATTTAACGTT	GATGTAATGG	AATTCCAGAT	3723
GTAGGCA1	rtc	CCCCCAGGTC	TTTTCATGTG	CAGATTGCAG	TTCTGATTCA	AAATAA	3783
AAGGAACT	rtg	GAAAAAAAA	A		•		3804

FIG.13

